

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Corley, Neil C.
Guegler, Karl G.
Lal, Preeti
Goli, Surya K.
Shah, Purvi
- (ii) TITLE OF THE INVENTION: DISEASE ASSOCIATED PROTEIN KINASES
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0321 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: HUVENOB01
 - (B) CLONE: 39043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Glu	Leu	Leu	Arg	Thr	Ile	Thr	Tyr	Gln	Pro	Ala	Ala	Ser	Thr	Lys
1				5				10					15		
Met	Cys	Glu	Gln	Ala	Leu	Gly	Lys	Gly	Cys	Gly	Ala	Asp	Ser	Lys	Lys
		20				25					30				
Lys	Arg	Pro	Pro	Gln	Pro	Pro	Glu	Glu	Ser	Gln	Pro	Pro	Gln	Ser	Gln

		35				40				45					
Ala	Gln	Val	Pro	Pro	Ala	Ala	Pro	His	His	His	His	His	His	Ser	His
50					55					60					
Ser	Gly	Pro	Glu	Ile	Ser	Arg	Ile	Ile	Val	Asp	Pro	Thr	Thr	Gly	Lys
65					70					75					80
Arg	Tyr	Cys	Arg	Gly	Lys	Val	Leu	Gly	Lys	Gly	Gly	Phe	Ala	Lys	Cys
				85					90					95	
Tyr	Glu	Met	Thr	Asp	Leu	Thr	Asn	Asn	Lys	Val	Tyr	Ala	Ala	Lys	Ile
			100					105					110		
Ile	Pro	His	Ser	Arg	Val	Ala	Lys	Pro	His	Gln	Arg	Glu	Lys	Ile	Asp
		115					120					125			
Lys	Glu	Ile	Glu	Leu	His	Arg	Ile	Leu	His	His	Lys	His	Val	Val	Gln
	130					135					140				
Phe	Tyr	His	Tyr	Phe	Glu	Asp	Lys	Glu	Asn	Ile	Tyr	Ile	Leu	Leu	Glu
145					150					155					160
Tyr	Cys	Ser	Arg	Arg	Ser	Met	Ala	His	Ile	Leu	Lys	Ala	Arg	Lys	Val
				165					170					175	
Leu	Thr	Glu	Pro	Glu	Val	Arg	Tyr	Tyr	Leu	Arg	Gln	Ile	Val	Ser	Gly
			180					185					190		
Leu	Lys	Tyr	Leu	His	Glu	Gln	Glu	Ile	Leu	His	Arg	Asp	Leu	Lys	Leu
		195					200					205			
Gly	Asn	Phe	Phe	Ile	Asn	Glu	Ala	Met	Glu	Leu	Lys	Val	Gly	Asp	Phe
	210				215						220				
Gly	Leu	Ala	Ala	Arg	Leu	Glu	Pro	Leu	Glu	His	Arg	Arg	Arg	Thr	Ile
225					230					235					240
Cys	Gly	Thr	Pro	Asn	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Asn	Lys	Gln	Gly
				245					250					255	
His	Gly	Cys	Glu	Ser	Asp	Ile	Trp	Ala	Leu	Gly	Cys	Val	Met	Tyr	Thr
			260					265					270		
Met	Leu	Leu	Gly	Arg	Pro	Pro	Phe	Glu	Thr	Thr	Asn	Leu	Lys	Glu	Thr
		275					280					285			
Tyr	Arg	Cys	Ile	Arg	Glu	Ala	Arg	Tyr	Thr	Met	Pro	Ser	Ser	Leu	Leu
	290					295					300				
Ala	Pro	Ala	Lys	His	Leu	Ile	Ala	Ser	Met	Leu	Ser	Lys	Asn	Pro	Glu
305					310					315					320
Asp	Arg	Pro	Ser	Leu	Asp	Asp	Ile	Ile	Arg	His	Asp	Phe	Phe	Leu	Gln
				325					330					335	
Gly	Phe	Thr	Pro	Asp	Arg	Leu	Ser	Ser	Ser	Cys	Cys	His	Thr	Val	Pro
			340					345					350		
Asp	Phe	His	Leu	Ser	Ser	Pro	Ala	Lys	Asn	Phe	Phe	Lys	Lys	Ala	Ala
		355					360					365			
Ala	Ala	Leu	Phe	Gly	Gly	Lys	Lys	Asp	Lys	Ala	Arg	Tyr	Ile	Asp	Thr
	370					375					380				
His	Asn	Arg	Val	Ser	Lys	Glu	Asp	Glu	Asp	Ile	Tyr	Lys	Leu	Arg	His
385					390					395					400
Asp	Leu	Lys	Lys	Thr	Ser	Ile	Thr	Gln	Gln	Pro	Ser	Lys	His	Arg	Thr
				405					410					415	
Asp	Glu	Glu	Leu	Gln	Pro	Pro	Thr	Thr	Thr	Val	Ala	Arg	Ser	Gly	Thr
			420					425					430		

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Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
435                               440                               445
Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
450                               455                               460
Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
465                               470                               475                               480
Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
485                               490                               495
Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
500                               505                               510
Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
515                               520                               525
Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Ala
530                               535                               540
His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
545                               550                               555                               560
Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
565                               570                               575
His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
580                               585                               590
Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
595                               600                               605
Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
610                               615                               620
Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625                               630                               635                               640
Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
645                               650                               655
Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
660                               665                               670
Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
675                               680                               685

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TBLYNOT01
- (B) CLONE: 40194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Pro Pro Lys Arg Asn Glu Lys Tyr Lys Leu Pro Ile Pro Phe Pro
1      5      10      15
Glu Gly Lys Val Leu Asp Asp Met Glu Gly Asn Gln Trp Val Leu Gly
20      25      30
Lys Lys Ile Gly Ser Gly Gly Phe Gly Leu Ile Tyr Leu Ala Phe Pro
35      40      45
Thr Asn Lys Pro Glu Lys Asp Ala Arg His Val Val Lys Val Glu Tyr
50      55      60
Gln Glu Asn Gly Pro Leu Phe Ser Glu Leu Lys Phe Tyr Gln Arg Val
65      70      75      80
Ala Lys Lys Asp Cys Ile Lys Lys Trp Ile Glu Arg Lys Gln Leu Asp
85      90      95
Tyr Leu Gly Ile Pro Leu Phe Tyr Gly Ser Gly Leu Thr Glu Phe Lys
100     105     110
Gly Arg Ser Tyr Arg Phe Met Val Met Glu Arg Leu Gly Ile Asp Leu
115     120     125
Gln Lys Ile Ser Gly Gln Asn Gly Thr Phe Lys Lys Ser Thr Val Leu
130     135     140

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Gln	Leu	Gly	Ile	Arg	Met	Leu	Asp	Val	Leu	Glu	Tyr	Ile	His	Glu	Asn	145	150	155	160
Glu	Tyr	Val	His	Gly	Asp	Val	Lys	Ala	Ala	Asn	Leu	Leu	Leu	Gly	Tyr	165	170	175	
Lys	Asn	Pro	Asp	Gln	Val	Tyr	Leu	Ala	Asp	Tyr	Gly	Leu	Ser	Tyr	Arg	180	185	190	
Tyr	Cys	Pro	Asn	Gly	Asn	His	Lys	Gln	Tyr	Gln	Glu	Asn	Pro	Arg	Lys	195	200	205	
Gly	His	Asn	Gly	Thr	Ile	Glu	Phe	Thr	Ser	Leu	Asp	Ala	His	Lys	Gly	210	215	220	
Val	Gly	Glu	Ile	Ala	Gln	Phe	Leu	Val	Cys	Ala	His	Ser	Leu	Ala	Tyr	225	230	235	240
Asp	Glu	Lys	Pro	Asn	Tyr	Gln	Ala	Leu	Lys	Lys	Ile	Leu	Asn	Pro	His	245	250	255	
Gly	Ile	Pro	Leu	Gly	Pro	Leu	Asp	Phe	Ser	Thr	Lys	Gly	Gln	Ser	Ile	260	265	270	
Asn	Val	His	Thr	Pro	Asn	Ser	Gln	Lys	Val	Asp	Ser	Gln	Lys	Ala	Ala	275	280	285	
Thr	Lys	Gln	Val	Asn	Lys	Ala	His	Asn	Arg	Leu	Ile	Glu	Lys	Lys	Val	290	295	300	
His	Ser	Glu	Arg	Ser	Ala	Glu	Ser	Cys	Ala	Thr	Trp	Lys	Val	Gln	Lys	305	310	315	320
Glu	Glu	Lys	Leu	Ile	Gly	Leu	Met	Asn	Asn	Glu	Ala	Ala	Gln	Glu	Ser	325	330	335	
Thr	Arg	Arg	Arg	Gln	Lys	Tyr	Gln	Glu	Ser	Gln	Glu	Pro	Leu	Asn	Glu	340	345	350	
Val	Asn	Ser	Phe	Pro	Gln	Lys	Ile	Ser	Tyr	Thr	Gln	Phe	Pro	Asn	Ser	355	360	365	
Phe	Tyr	Glu	Pro	His	Gln	Asp	Phe	Thr	Ser	Pro	Asp	Ile	Phe	Lys	Lys	370	375	380	
Ser	Arg	Ser	Pro	Ser	Trp	Tyr	Lys	Tyr	Thr	Ser	Thr	Val	Ser	Thr	Gly	385	390	395	400
Ile	Thr	Asp	Leu	Glu	Ser	Ser	Thr	Gly	Leu	Trp	Pro	Thr	Ile	Ser	Gln	405	410	415	
Phe	Thr	Leu	Ser	Glu	Glu	Thr	Asn	Ala	Asp	Val	Tyr	Tyr	Tyr	Arg	Ile	420	425	430	
Ile	Ile	Pro	Val	Leu	Leu	Met	Leu	Val	Phe	Leu	Ala	Leu	Phe	Phe	Leu	435	440	445	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TMLR3DT01
- (B) CLONE: 402339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Leu	Ala	Arg	Arg	Lys	Pro	Val	Leu	Pro	Ala	Leu	Thr	Ile	Asn	Pro	1	5	10	15
Thr	Ile	Ala	Glu	Gly	Pro	Ser	Pro	Thr	Ser	Glu	Gly	Ala	Ser	Glu	Ala	20	25	30	
Asn	Leu	Val	Asp	Leu	Gln	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Leu	Asp	Glu	35	40	45	
Gln	Gln	Lys	Lys	Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Ala	Lys	Val	50	55	60	
Gly	Glu	Leu	Lys	Asp	Asp	Asp	Phe	Glu	Arg	Ile	Ser	Glu	Leu	Gly	Ala	65	70	75	80
Gly	Asn	Gly	Gly	Val	Val	Thr	Lys	Val	Gln	His	Arg	Pro	Ser	Gly	Leu	85	90	95	

Ile	Met	Ala	Arg	Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Ile	Arg
			100					105					110		
Asn	Gln	Ile	Ile	Arg	Glu	Leu	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro
		115					120					125			
Tyr	Ile	Val	Gly	Phe	Tyr	Gly	Ala	Phe	Tyr	Ser	Asp	Gly	Glu	Ile	Ser
	130					135					140				
Ile	Cys	Met	Glu	His	Met	Asp	Gly	Gly	Ser	Leu	Asp	His	Leu	Leu	Lys
145					150					155					160
Glu	Ala	Lys	Arg	Ile	Pro	Glu	Glu	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala
			165						170					175	
Val	Leu	Arg	Gly	Leu	Ala	Tyr	Leu	Arg	Glu	Lys	His	Gln	Ile	Met	His
			180					185					190		
Arg	Asp	Val	Lys	Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile
		195				200					205				
Lys	Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala
	210				215						220				
Asn	Ser	Phe	Val	Gly	Thr	Arg	Ser	Tyr	Met	Ala	Pro	Glu	Arg	Leu	Gln
225					230					235					240
Gly	Thr	His	Tyr	Ser	Val	Gln	Ser	Asp	Ile	Trp	Ser	Met	Gly	Leu	Ser
			245					250					255		
Leu	Val	Glu	Leu	Ala	Val	Gly	Arg	Tyr	Pro	Ile	Pro	Pro	Pro	Asp	Ala
			260					265					270		
Lys	Glu	Leu	Glu	Ala	Ile	Phe	Gly	Arg	Pro	Val	Val	Asp	Gly	Glu	Glu
	275					280						285			
Gly	Glu	Pro	His	Ser	Ile	Ser	Pro	Arg	Pro	Arg	Pro	Pro	Gly	Arg	Pro
	290					295					300				
Val	Ser	Gly	His	Gly	Met	Asp	Ser	Arg	Pro	Ala	Met	Ala	Ile	Phe	Glu
305					310					315					320
Leu	Leu	Asp	Tyr	Ile	Val	Asn	Glu	Pro	Pro	Pro	Lys	Leu	Pro	Asn	Gly
			325					330					335		
Val	Phe	Thr	Pro	Asp	Phe	Gln	Glu	Phe	Val	Asn	Lys	Cys	Leu	Ile	Lys
			340					345					350		
Asn	Pro	Ala	Glu	Arg	Ala	Asp	Leu	Lys	Met	Leu	Thr	Asn	His	Thr	Phe
		355				360						365			
Ile	Lys	Arg	Ser	Glu	Val	Glu	Glu	Val	Asp	Phe	Ala	Gly	Trp	Leu	Cys
	370				375					380					
Lys	Thr	Leu	Arg	Leu	Asn	Gln	Pro	Gly	Thr	Pro	Thr	Arg	Thr	Ala	Val
385					390					395					400

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT04
- (B) CLONE: 705365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Met	Thr	Ala	Gly	Thr	Thr	Thr	Thr	Phe	Pro	Met	Ser	Asn	His
1				5					10					15	
Thr	Arg	Glu	Arg	Val	Thr	Val	Ala	Lys	Leu	Thr	Leu	Glu	Asn	Phe	Tyr
			20					25					30		
Ser	Asn	Leu	Ile	Leu	Gln	His	Glu	Glu	Arg	Glu	Thr	Arg	Gln	Lys	Lys
	35					40						45			
Leu	Glu	Val	Ala	Met	Glu	Glu	Gly	Leu	Ala	Asp	Glu	Glu	Lys	Lys	
	50				55					60					
Leu	Arg	Arg	Ser	Gln	His	Ala	Arg	Lys	Glu	Thr	Glu	Phe	Leu	Arg	Leu
65					70					75					80
Lys	Arg	Thr	Arg	Leu	Gly	Leu	Asp	Asp	Phe	Glu	Ser	Leu	Lys	Val	Ile
			85					90						95	
Gly	Arg	Gly	Ala	Phe	Gly	Glu	Val	Arg	Leu	Val	His	Lys	Lys	Asp	Thr

[illegible][illegible][illegible]

- | | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
|---|---|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| 0 | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |

[illegible]

- [illegible]

[illegible][illegible]

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Lys Ala Leu Arg Gly Lys Glu Ala Leu Val Glu Asn Glu Ile Ala Val
50      55      60
Leu Arg Arg Ile Ser His Pro Asn Ile Val Ala Leu Glu Asp Val His
65      70      75      80
Glu Ser Pro Ser His Leu Tyr Leu Ala Met Glu Leu Val Thr Gly Gly
85      90      95
Glu Leu Phe Asp Arg Ile Met Glu Arg Gly Ser Tyr Thr Glu Lys Asp
100     105     110
Ala Ser His Leu Val Gly Gln Val Leu Gly Ala Val Ser Tyr Leu His
115     120     125
Ser Leu Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Tyr
130     135     140
Ala Thr Pro Phe Glu Asp Ser Lys Ile Met Val Ser Asp Phe Gly Leu
145     150     155     160
Ser Lys Ile Gln Ala Gly Asn Met Leu Gly Thr Ala Cys Gly Thr Pro
165     170     175
Gly Tyr Val Ala Pro Glu Leu Leu Glu Gln Lys Pro Tyr Gly Lys Ala
180     185     190
Val Asp Val Trp Ala Leu Gly Val Ile Ser Tyr Ile Leu Leu Cys Gly
195     200     205
Tyr Pro Pro Phe Tyr Asp Glu Ser Asp Pro Glu Leu Phe Ser Gln Ile
210     215     220
Leu Arg Ala Ser Tyr Glu Phe Asp Xaa Pro Phe Trp Asp Asp Ile Ser
225     230     235     240
Glu Ser Gly Lys Asp Phe Ile Arg His Leu Leu Glu Arg Asp Leu Gln
245     250     255
Lys Arg Phe Thr Cys Gln Gln Ala Leu Arg Asp Leu Trp Ile Phe Trp
260     265     270
Asp Thr Gly Phe Gly Arg Asp Ile Leu Gly Phe Val Ser Glu Gln Ile
275     280     285
Arg Lys Asn Phe Ala Trp Thr His Trp Lys Arg Ala Phe Asn Ala Thr
290     295     300
Leu Phe Leu Arg His Ile Arg Lys Leu Gly Gln Ile Pro Glu Gly Glu
305     310     315     320
Gly Ala Ser Glu Gln Gly Met Xaa Arg His Ser His Xaa Gly Leu Arg
325     330     335
Ala Gly Gln Pro Pro Lys Trp
340

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT03
- (B) CLONE: 1340712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Ile Leu Ala Ser Val Leu Arg Ser Gly Pro Gly Gly Gly Leu Pro
1      5      10      15
Leu Arg Pro Leu Leu Gly Pro Ala Leu Ala Leu Arg Ala Arg Ser Thr
20     25     30
Ser Ala Thr Asp Thr His His Val Glu Met Ala Arg Glu Arg Ser Lys
35     40     45
Thr Val Thr Ser Phe Tyr Asn Gln Ser Ala Ile Asp Ala Ala Ala Glu
50     55     60
Lys Pro Ser Val Arg Leu Thr Pro Thr Met Met Leu Tyr Ala Gly Arg
65     70     75     80
Ser Gln Asp Gly Ser His Leu Leu Lys Ser Ala Arg Tyr Leu Gln Gln
85     90     95

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Glu Leu Pro Val Arg Ile Ala His Arg Ile Lys Gly Phe Arg Cys Leu
 100 105 110
 Pro Phe Ile Ile Gly Cys Asn Pro Thr Ile Leu His Val His Glu Leu
 115 120 125
 Tyr Ile Arg Ala Phe Gln Lys Leu Thr Asp Phe Pro Pro Ile Lys Asp
 130 135 140
 Gln Ala Asp Glu Ala Gln Tyr Cys Gln Leu Val Arg Gln Leu Leu Asp
 145 150 155 160
 Asp His Lys Asp Val Val Thr Leu Leu Ala Glu Gly Leu Arg Glu Ser
 165 170 175
 Arg Lys His Ile Glu Asp Glu Lys Leu Val Arg Tyr Phe Leu Asp Lys
 180 185 190
 Thr Leu Thr Ser Arg Leu Gly Ile Arg Met Leu Ala Thr His His Leu
 195 200 205
 Ala Leu His Glu Asp Lys Pro Asp Phe Val Gly Ile Ile Cys Thr Arg
 210 215 220
 Leu Ser Pro Lys Lys Ile Ile Glu Lys Trp Val Asp Phe Ala Arg Arg
 225 230 235 240
 Leu Cys Glu His Lys Tyr Gly Asn Ala Pro Arg Val Arg Ile Asn Gly
 245 250 255
 His Val Ala Ala Arg Phe Pro Phe Ile Pro Met Pro Leu Asp Tyr Ile
 260 265 270
 Leu Pro Glu Leu Leu Lys Asn Ala Met Arg Ala Thr Met Glu Ser His
 275 280 285
 Leu Asp Thr Pro Tyr Asn Val Pro Asp Val Val Ile Thr Ile Ala Asn
 290 295 300
 Asn Asp Val Asp Leu Ile Ile Arg Ile Ser Asp Arg Gly Gly Gly Ile
 305 310 315 320
 Ala His Lys Asp Leu Asp Arg Val Met Asp Tyr His Phe Thr Thr Ala
 325 330 335
 Glu Ala Ser Thr Gln Asp Pro Arg Ile Ser Pro Leu Phe Gly His Leu
 340 345 350
 Asp Met His Ser Gly Ala Gln Ser Gly Pro Met His Gly Phe Gly Phe
 355 360 365
 Gly Leu Pro Thr Ser Arg Ala Tyr Ala Glu Tyr Leu Gly Gly Ser Leu
 370 375 380
 Gln Leu Gln Ser Leu Gln Gly Ile Gly Thr Asp Val Tyr Leu Arg Leu
 385 390 395 400
 Arg His Ile Asp Gly Arg Glu Glu Ser Phe Arg Ile
 405 410

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENITUT01
- (B) CLONE: 1452972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Leu Glu Lys Leu Glu Phe Glu Asp Glu Ala Val Glu Asp Ser Glu
 1 5 10 15
 Ser Gly Val Tyr Met Arg Phe Met Arg Ser His Lys Cys Tyr Asp Ile
 20 25 30
 Val Pro Thr Ser Ser Lys Leu Val Val Phe Asp Thr Thr Leu Gln Val
 35 40 45
 Lys Lys Ala Phe Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro
 50 55 60

Leu Trp Glu Ser Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr
 65 70 75 80
 Asp Phe Ile Asn Ile Leu His Arg Tyr Tyr Lys Ser Pro Met Val Gln
 85 90 95
 Ile Tyr Glu Leu Glu Glu His Lys Ile Glu Thr Trp Arg Glu Leu Tyr
 100 105 110
 Leu Gln Glu Thr Phe Lys Pro Leu Val Asn Ile Ser Pro Asp Ala Ser
 115 120 125
 Leu Phe Asp Ala Val Tyr Ser Leu Ile Lys Asn Lys Ile His Arg Leu
 130 135 140
 Pro Val Ile Asp Pro Ile Ser Gly Asn Ala Leu Tyr Ile Leu Thr His
 145 150 155 160
 Lys Arg Ile Leu Lys Phe Leu Gln Leu Phe Met Ser Asp Met Pro Lys
 165 170 175
 Pro Ala Phe Met Lys Gln Asn Leu Asp Glu Leu Gly Ile Gly Thr Tyr
 180 185 190
 His Asn Ile Ala Phe Ile His Pro Asp Thr Pro Ile Ile Lys Ala Leu
 195 200 205

 Asn Ile Phe Val Glu Arg Arg Ile Ser Ala Leu Pro Val Val Asp Glu
 210 215 220
 Ser Gly Lys Val Val Asp Ile Tyr Ser Lys Phe Asp Val Ile Asn Leu
 225 230 235 240
 Ala Ala Glu Lys Thr Tyr Asn Asn Leu Asp Ile Thr Val Thr Gln Ala
 245 250 255
 Leu Gln His Arg Ser Gln Tyr Phe Glu Gly Val Val Lys Cys Asn Lys
 260 265 270
 Leu Glu Ile Leu Glu Thr Ile Val Asp Arg Ile Val Arg Ala Glu Val
 275 280 285
 His Arg Leu Val Val Val Asn Glu Ala Asp Ser Ile Val Gly Ile Ile
 290 295 300
 Ser Leu Ser Asp Ile Leu Gln Ala Leu Ile Leu Thr Pro Ala Gly Ala
 305 310 315 320
 Lys Gln Lys Glu Thr Glu Thr Glu
 325

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2770 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVENOB01
 (B) CLONE: 39043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAGTCGGCAC	CAGAGGCAAG	GGTGCGAGGA	CCACGGCCGG	CTCGGACGTG	TGACCGCGCC	60
TAGGGGGTGG	CAGCGGGCAG	TGCGGGGCGG	CAAGGCGACC	ATGGAGCTTT	TGCGGACTAT	120
CACCTACCAG	CCAGCCGCCA	GCACCAAAAT	GTGCGAGCAG	GCGCTGGGCA	AGGTTGCGG	180
AGCGGACTCG	AAGAAGAAGC	GGCCGCCGCA	GCCCCCGAG	GAATCGCAGC	CACCTCAGTC	240
CCAGGCGCAA	GTGCCCCCGG	CGGCCCTCA	CCACCATCAC	CACCATTCGC	ACTCGGGGCC	300
GGAGATCTCG	CGGATTATCG	TCGACCCAC	GACTGGGAAG	CGCTACTGCC	GGGGCAAAGT	360
GCTGGGAAAG	GGTGGCTTTG	CAAAATGTTA	CGAGATGACA	GATTTGACAA	ATAACAAAGT	420
CTACGCCGCA	AAAATTATTC	CTCACAGCAG	AGTAGCTAAA	CCTCATCAAA	GGGAAAAGAT	480
TGACAAAGAA	ATAGAGCTTC	ACAGAATTCT	TCATCATAAG	CATGTAGTGC	AGTTTTACCA	540
CTACTTCGAG	GACAAAGAAA	ACATTTACAT	TCTCTTGGA	TACTGCAGTA	GAAGGTCAAT	600
GGCTCATATT	TTGAAAGCAA	GAAAGGTGTT	GACAGAGCCA	GAAGTTCGAT	ACTACCTCAG	660
GCAGATTGTG	TCTGGACTGA	AATACCTTCA	TGAACAAGAA	ATCTTGCACA	GAGATCTCAA	720
ACTAGGGAAC	TTTTTTATTA	ATGAAGCCAT	GGAACATAAA	GTTGGGGACT	TCGGTCTGGC	780
AGCCAGGCTA	GAACCTTTGG	AACACAGAAG	GAGAACGATA	TGTGGTACCC	CAAATTATCT	840
CTCTCCTGAA	GTCCTCAACA	AACAAGGACA	TGGCTGTGAA	TCAGACATTT	GGGCCCTGGG	900
CTGTGTAATG	TATACAATGT	TACTAGGGAG	GCCCCCATTT	GAAACTACAA	ATCTCAAAGA	960

AACTTATAGG	TGCATAAGGG	AAGCAAGGTA	TACAATGCCG	TCCTCATTGC	TGGCTCCTGC	1020
CAAGCACTTA	ATTGCTAGTA	TGTTGTCCAA	AAACCCAGAG	GATCGTCCCA	GTTTGGATGA	1080
CATCATTCGA	CATGACTTTT	TTTTGCAGGG	CTTCACTCCG	GACAGACTGT	CTTCTAGCTG	1140
TTGTCATACA	GTTCCAGATT	TCCACTTATC	AAGCCCAGCT	AAGAATTTCT	TTAAGAAAGC	1200
AGCTGCTGCT	CTTTTTGGTG	GCAAAAAAGA	CAAAGCAAGA	TATATTGACA	CACATAATAG	1260
AGTGTCTAAA	GAAGATGAAG	ACATCTACAA	GCTTAGGCAT	GATTTGAAAA	AGACTTCAAT	1320
AACTCAGCAA	CCCAGCAAAC	ACAGGACAGA	TGAGGAGCTC	CAGCCACCTA	CCACCACAGT	1380
TGCCAGGTCT	GGAACACCCG	CAGTAGAAAA	CAAGCAGCAG	ATTGGGGATG	CTATTCCGAT	1440
GATAGTCAGA	GGGACTCTTG	GCAGCTGTAG	CAGCAGCAGT	GAATGCCTTG	AAGACAGTAC	1500
CATGGGAAGT	GTTGCAGACA	CAGTGGCAAG	GGTCTTTCGG	GGATGTCTGG	AAAACATGCC	1560
GGAAGCTGAT	TGCATTCCTA	AAGAGCAGCT	GAGCACATCA	TTTCAGTGGG	TCACCAAATG	1620
GGTTGATTAC	TCTAACAAAT	ATGGCTTTGG	GTACCAGCTC	TCAGACCACA	CCGTCGGTGT	1680
CCTTTTCAAC	AATGGTGCTC	ACATGAGCCT	CCTTCCAGAC	AAAAAACACAG	CTCACTATTA	1740
CGCAGAGCTT	GGCCAATGCT	CAGTTTTCCC	AGCAACAGAT	GCTCCTGAGC	AATTTATTAG	1800
TCAAGTGACG	GTGCTGAAAT	ACTTTTCTCA	TTACATGGAG	GAGAACCTCA	TGGATGGTGG	1860
AGATCTGCCCT	AGTGTTACTG	ATATTGGAAG	ACCTCGGCTC	TACCTCCTTC	AGTGGCTAAA	1920
ATCTGATAAG	GGCCTAATGA	TGCTCTTTAA	TGATGGCACC	TTTCAGGTGA	ATTTCTACCA	1980
TGATCATACA	AAAATCATCA	TCTGTAGCCA	AAATGAAGAA	TACCTTCTCA	CCTACATCAA	2040
TGAGGATAGG	ATATCTACAA	CTTTCAGGCT	GACAACTCTG	CTGATGTCTG	GCTGTTCATC	2100
AGAATTAAAA	AATCGAATGG	AATATGCCCT	GAACATGCTC	TTACAAAGAT	GTAAGTAAAA	2160
GACTTTTTCGA	ATGGACCCTA	TGGGACTCCT	CTTTTCCACT	GTGAGATCTA	CAGGGGAAGCC	2220
AAAAGAATGA	TCTAGAGTAT	GTTGAAGAAG	ATGGACATGT	GGTGGTACGA	AAACAATTCC	2280
CCTGTGGCCT	GCTGGACTGG	GTGGAACGAG	AACAGGCTAA	GGCATAACAGT	TCTTGACTTT	2340
GGACAATCCA	AGAGTGAACC	AGAATGCAGT	TTTCCTTGAG	ATACCTGTTT	TAAAAGGTTT	2400
TTTCAAGCAAT	TTTGCAGAAA	GGTGCATTGA	TTCTTAAATT	CTCTCTGTTG	AGAGCATTTT	2460
AGCCAGAGGA	CTTTGGAAGT	GTGAATATAC	TTCTTGAAGG	GGAGGGAGAA	GGGAGGAAGC	2520
TCCCATGTTG	TTTAAAGGCT	GTAATTGGAG	CAGCTTTTGG	CTGCGTAACT	GTGAAGTATG	2580
GCCATATATA	ATTTT'TTTT	ATTAATTTT	GAAGATACTT	GTGGCTGGAA	AAGTGCATTC	2640
CTTGTTAATA	AACTTTT'TAT	TTATTACAGC	CCAAAGAGCA	GTATTTATTA	TCAAAATGTC	2700
TTTTTTT'TTA	TGTTGACCAT	TTTAAACCGT	TGGCAATAAA	GAGTATGAAA	ACGCAGAAAA	2760
AAAAAAAAAA						2770

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TBLYN0T01
- (B) CLONE: 40194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAGGCGTCC	CCTTCTACTC	ACGTTTGCCA	AAAGCGGGTC	CGACGTGTTA	GCGGAAAAAA	60
GTGATGCCAC	CAAAAAGAAA	TGAAAAATAC	AAACTTCCTA	TTCCATTTCC	AGAAGGCAAG	120
GTTCTGGATG	ATATGGAAGG	CAATCAGTGG	GTACTGGGCA	AGAAGATTGG	CTCTGGAGGA	180
TTTGGATTGA	TATATTTAGC	TTTCCCCACA	AATAAACCCAG	AGAAAGATGC	AAGACATGTA	240
GTAAGAGTGG	AATATCAAGA	AAATGGCCCG	TTATTTTTCAG	AACTTAAATT	TTATCAGAGA	300
GTTGCAAAAA	AAGACTGTAT	CAAAAAGTGG	ATAGAACGCA	AACAACCTGA	TTATTTAGGA	360
ATTCCTCTGT	TTTATGGATC	TGGTCTGACT	GAATTCAAGG	GAAGAAGTTA	CAGATTTATG	420
GTAATGGAAA	GACTAGGAAT	AGATTTACAG	AAGATCTCAG	GCCAGAATGG	TACCTTTAAA	480
AAGTCAACTG	TCCTGCAATT	AGGTATCCGA	ATGTTGGATG	TACTGGAATA	TATACATGAA	540
AATGAATATG	TTTATGGTGA	TGTAAAAGCA	GCAAATCTAC	TTTTGGGTTA	CAAAAATCCA	600
GACCAGGTTT	ATCTTGCAGA	TTATGGACTT	TCCTACAGAT	ATTGTCCCAA	TGGGAACCAC	660
AAACAGTATC	AGGAAAATCC	TAGAAAAGGC	CATAATGGGA	CAATAGAGTT	TACCAGCTTG	720
GATGCCCCAC	AGGGAGTAGG	TGAAATAGCC	CAATTTT'TTG	TATGTGCTCA	TAGTTTAGCA	780
TATGATGAAA	AGCCAAACTA	TCAAGCCCTC	AAGAAAATTT	TGAACCCTCA	TGGAATACCT	840
TTAGGACCAC	TGGACTTTTC	CAGAAAAGGA	CAGAGTATAA	ATGTCCATAC	TCCAAACAGT	900
CAAAAAGTTG	ATTCACAAAA	GGCTGCAACA	AAGCAAGTCA	ACAAGGCACA	CAATAGGTTA	960
ATCGAAAAAA	AAGTCCACAG	TGAGAGAAGC	GCTGAGTCCT	GTGCAACATG	GAAAGTGCAG	1020
AAAGAGGAGA	AACTGATTGG	ATTGATGAAC	AATGAAGCAG	CTCAGGAAAG	CACAAGGAGA	1080
AGACAGAAAT	ATCAAGAGTC	TCAAGAACCT	TTGAATGAAG	TAAACAGTTT	CCCACAAAAA	1140
ATCAGCTATA	CACAATTCCC	AAACTCATT	TATGAGCCTC	ATCAAGATTT	TACCAGTCCA	1200

GATATATTCA	AGAAGTCAAG	ATCTCCATCT	TGGTATAAAT	ACACTTCCAC	AGTCAGCACG	1260
GGGATCACAG	ACTTAGAAAG	TTCAACTGGA	CTTTGGCCCTA	CAATTTCCCA	GTTTACTCTT	1320
AGTGAAGAGA	CAAACGCAGA	TGTTTATTAT	TATCGCATCA	TCATACCTGT	CCTTTTGATG	1380
TTAGTATTTT	TTGCTTTTAT	TTTTCTCTGA	AGATGATACC	AAAATTCCTT	TTGATAATTT	1440
TTTAAGTTTC	CAGCTCTTCA	CCGAAATGTT	GTATTCCTTAT	TTCAGTGTTC	CCTTCCAGAC	1500
ATTTTAAAGG	TAATTGGCTT	TAAAAAGAGA	ACATATTTTA	ACAAAGTTTG	TGGACACTCT	1560
AAAAAATAAA	ATTGCTTTGT	ACTAGAAAAA	AAA			1593

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TMLR3DT01
- (B) CLONE: 402339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGCCCCGCG	GAGCCCCGAT	GCTGGCCCCG	AGGAAGCCGG	TGCTGCCGGC	GCTCACCATC	60
AACCCTACCA	TCGCCGAGGG	CCCATCCCCT	ACCAGCGAGG	GCGCCTCCGA	GGCAAACCTG	120
GTGGACCTGC	AGAAGAAGCT	GGAGGAGCTG	GAACCTGACG	AGCAGCAGAA	GAAGCGGCTG	180
GAAGCCTTTC	TCACCCAGAA	AGCCAAGGTC	GGCGAACTCA	AAGACGATGA	CTTCGAAAGG	240
ATCTCAGAGC	TGGGCGCGGG	CAACGGCGGG	GTGGTCACCA	AAGTCCAGCA	CAGACCCTCG	300
GGCCTCATCA	TGGCCAGGAA	GCTGATCCAC	CTTGAGATCA	AGCCGGCCAT	CCGGAACCAG	360
ATCATCCGCG	AGCTGCAGGT	CCTGCACGAA	TGCAACTCGC	CGTACATCGT	GGGCTTCTAC	420
GGGGCCTTCT	ACAGTGACGG	GGAGATCAGC	ATTTGTCATG	AACACATGGA	CGGCGGCTCC	480
CTGGACCATC	TGCTGAAAGA	GGCCAAGAGG	ATTCCCAGAG	AGATCCTGGG	GAAAGTCAGC	540
ATCGCGGTTT	TCCGGGGCTT	GGCGTACCTC	CGAGAGAAGC	ACCAGATCAT	GCACCGAGAT	600
GTGAAGCCCT	CCAACATCCT	CGTGAACCTC	AGAGGGGAGA	TCAAGCTGTG	TGACTTCGGG	660
GTGAGCGGCC	AGCTCATCGA	CTCCATGGCC	AACTCCTTCG	TGGGCACGCG	CTCCTACATG	720
GCTCCGGAGC	GGTTGCAGGG	CACACATTAC	TCGGTGCAGT	CGGACATCTG	GAGCATGGGC	780
CTGTCCCTGG	TGGAGCTGGC	CGTCGGAAGG	TACCCCATCC	CCCCGCCCCG	CGCCAAAGAG	840
CTGGAGGCCA	TCTTTGGCCG	GCCCGTGGTC	GACGGGGAAG	AAGGAGAGCC	TCACAGCATC	900
TCGCCTCGGC	CGAGGCCCCC	CGGGCGCCCC	GTCAGCGGTC	ACGGGATGGA	TAGCCGGCCT	960
GCCATGGCCA	TCTTTGAACT	CCTGGACTAT	ATTGTGAACG	AGCCACCTCC	TAAGCTGCCC	1020
AACGGTGTGT	TCACCCCCGA	CTTCCAGGAG	TTTGTCAATA	AATGCCTCAT	CAAGAACCCA	1080
GCGGAGCGGG	CGGACCTGAA	GATGCTCACA	AACCACACCT	TCATCAAGCG	GTCCGAGGTG	1140
GAAGAAGTGG	ATTTTGCCGG	CTGGTTGTGT	AAAACCCCTG	GGCTGAACCA	GCCCGGCACA	1200
CCCACGCGCA	CCGCCGTGTG	ACAGTGGCCG	GGCTCCCTGC	GTCCCGCTGG	TGACCTGCCC	1260
ACCGTCCCTG	TCCATGCCCC	GCCCTTCCAG	CTGAGGACAG	GCTGGCGCCT	CCACCCACCC	1320
TCTTGCTTCA	CCCCTGCGGA	GAGCACCGTG	GCGGGGCGAC	AGCGCATGCA	GGAACGGGGG	1380
TCTCTCTCTC	TGCCCGTCCT	GGCCGGGGTG	CCTCTGGGGA	CGGGCGACGC	TGCTGTGTGT	1440
GGTCTCAGAG	GCTCTGCTTC	CTTAGGTTAC	AAAACAAAAC	AGGGAGAGAA	AAAGCAAAAA	1500
AAAA						1504

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1935 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT04
- (B) CLONE: 705365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGAGGCTG	AGCCGGCCGC	GGGCGCGACC	GGAGGCAGTT	TCCGTTACTA	TGGCAATGAC	60
GGCAGGGACT	ACAACAACCT	TTCCTATGAG	CAACCATACC	CGGGAAAGAG	TGACTGTAGC	120
CAAGCTCACA	TTGGAGAATT	TTTATAGCAA	CCTAATTTTA	CAGCATGAAG	AGAGAGAAAC	180

CAGGCAGAAG	AAATTAGAAG	TGGCCATGGA	AGAAGAAGGA	TTAGCAGATG	AAGAGAAAAA	240
GTTACGTCGA	TCACAACACG	CTCGCAAAGA	AACAGAGTTC	TTACGGCTCA	AAAGGACCAG	300
ACTTGGCTTG	GATGACTTTG	AGTCTCTGAA	AGTTATAGGA	AGAGGAGCTT	TTGGAGAGGT	360
GCGGTTGGTC	CACAAAAAAG	ATACAGGCCA	TATCTATGCA	ATGAAGATAT	TGAGAAAGTC	420
TGATATGCTT	GAAAAAGAGC	AGGTGGCCCA	TATCCGAGCA	GAAAGAGATA	TTTTGGTAGA	480
AGCAGATGGT	GCCTGGGTGG	TGAAGATGTT	TTACAGTTTT	CAGGATAAGA	GGAATCTTTA	540
TCTAATCATG	GAATTTCTCC	CTGGAGGTGA	CATGATGACA	TTGCTAATGA	AGAAAGACAC	600
CTTGACAGAA	GAGGAAACAC	AGTTCTACAT	TTCAGAGACT	GTTCCTGGCAA	TAGATGCGAT	660
CCACCAGTTG	GGTTTCATCC	ATCGGGATAT	TAAGCCAGAC	AACCTTTTAT	TGGATGCCAA	720
GGGTCAATGA	AAATTATCTG	ATTTTGGTTC	ATGTACGGGA	TTAAAGAAAG	CTCACAGGAC	780
TGAATTTTAT	AGAAATCTCA	CACACAACCC	ACCAAGTGAC	TTCTCATTTT	AGAACATGAA	840
CTCAAAGAGG	AAAGCAGAAA	CTTGGAAGAA	GAACAGGAGA	CAACTGGCAT	ATTCCACAGT	900
TGGGACACCA	GATTACATTG	CTCCAGAAGT	ATTCATGCAG	ACTGGTTACA	ACAAATTGTG	960
TGACTGGTGG	TCTTTGGGAG	TGATTATGTA	TGAAATGCTA	ATAGGATATC	CACCTTTCTG	1020
CTCTGAAACA	CCTCAAGAAA	CATACAGAAA	AGTGATGAAC	TGGAAAGAAA	CTCTGGTATT	1080
TTCTCCAGAG	GTACCTATAT	CTGAGAAAGC	CAAGGACTTA	ATTCTCAGAT	TTTGTATTGA	1140
TTCTGAAAAC	AGAATTGGAA	ATAGTGGAGT	AGAAGAAATA	AAAGGTCATC	CCTTTTGTGA	1200
AGGTGTCGAC	TGGGAGCACA	TAAGGGAAAG	GCCAGCAGCA	ATCCCTATAG	AAATCAAAAAG	1260
CATTGATGAT	ACTTCAAATT	TTGATGACTT	CCCTGAATCT	GATATTTTAC	AACCAGTGCC	1320
AAATACCACA	GAACCGGACT	ACAAATCCAA	AGACTGGGTT	TTTCTCAATT	ATACCTATAA	1380
AAGGTTTGAA	GGGTTGACTC	AACGTGGCTC	TATCCCCACC	TACATGAAAG	CTGGGAAGTT	1440
ATGAATGAAG	ATAACATTCA	CCCATAACCA	AGAGAACTCA	GGTAGCTGCA	TCACCAGGCT	1500
TGCTTGCGCT	AGATAACAAT	ACACTGAAAT	ACTCCTGAAG	ATGGTGGTGC	TTATTGACTA	1560
CAAGAGGAAA	TTCTACAGGA	TTAGGATTTT	TAAGACTACT	ATAGGAATTG	GTTGGCAGTG	1620
CCAGCTGGCT	CTTTTTTTTT	ATATTTTATT	ATTTTGTGTT	ACTTTATTAT	ATGAAGGTAC	1680
TGGAATAAAA	GGAACAGACA	TCCCTTTCTA	ACTGCACCTG	CTACATGCGT	ATTAAGGTCC	1740
ATTCTGCCTG	TGTGTGCTGT	GGCTTTGAAC	TGTAACACCT	CTAATCAATT	CAGGAGAAAC	1800
ACATATCATT	TAAAGCAACA	TAGGCTAACC	TGTANGTAAC	ACTGCAGTAT	TGATGTTTTA	1860
CTGCAAACT	TATGGGTCTA	GATAATCAGT	AAAAGCCATC	TTCCATAGTT	GGTGTTAGAA	1920
CATTGCCCTA	TTGGT					1935

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT06
- (B) CLONE: 827431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAAGTTTCTC	ACTAGGGTCT	TCTCTGGCCC	AGCCTTTGAC	TGAAGCTGGT	CTGGAGACAG	60
GGGCATTAGA	GAAGTGA CTC	ATAGATGGCC	TAAAGAAGCG	GGGCCACTCA	AGGACCCAGG	120
ACAGAGGGAA	GAGGGCCAAC	CCAGCTGGAC	CACAGGCCAAA	CCCCATTGCC	TTTGAGAGAA	180
AGAAGAGGAC	CCGGTGAAAC	ATGCTGCTGC	TGAAGAAACA	CACGGAGGAC	ATCAGCAGCG	240
TCTACGAGAT	CCGCGAGAGG	CTCGGCTCGG	GTGCCTTCTC	CGAGGTGGTG	CTGGCCCAGG	300
AGCGGGGCTC	CGCACACCTC	GTGGCCCTCA	AGTGCATCCC	CAAGAAGGCC	CTCCGGGGCA	360
AGGAGGCCCT	GGTGGAGAAC	GAGATCGCAG	TGCTCCGTAG	GATCAGTCAC	CCCAACATCG	420
TCGCTCTGGA	GGATGTCCAC	GAGAGCCCTT	CCCACCTCTA	CCTGGCCATG	GAAGTGGTGA	480
CGGGTGGCGA	GCTGTTTGAC	CGCATCATGG	AGCGCGGCTC	CTACACAGAG	AAGGATGCCA	540
GCCATCTGGT	GGGTCAGGTC	CTTGCGCCCG	TCTCCTACCT	GCACAGCCTG	GGGATCGTGC	600
ACCGGGACCT	CAAGCCCGAA	AACCTCCTGT	ATGCCACGCC	CTTTGAGGAC	TCGAAGATCA	660
TGGTCTCTGA	CTTTGGACTC	TCCAAAATCC	AGGCTGGGAA	CATGCTAGGC	ACCGCCTGTG	720
GGACCCCTGG	ATATGTGGCC	CCAGAGCTCT	TGGAGCAGAA	ACCCTACGGG	AAGGCCGTAG	780
ATGTGTGGGC	CCTGGGCGTC	ATCTCCTACA	TCCTGCTGTG	TGGGTACCCC	CCCTTCTACG	840
ACGAGAGCGA	CCCTGAGCTC	TTCAGCCAGA	TCCTGAGGGC	CAGCTATGAG	TTTGACTNTC	900
CTTTCTGGGA	TGACATCTCA	GAATCAGGCA	AAGACTTTAT	TCGGCACCTT	CTGGAGCGAG	960
ACCTTCAGAA	GAGGTTTACC	TGCCAACAGG	CCTTGCGGGA	CCTTTGGATC	TTTTGGGACA	1020
CAGGCTTTGG	CAGGGACATC	TTAGGGTTTG	TCAGTGAGCA	GATCCGGAAG	AACTTTGCTT	1080
GGACACACTG	GAAGCGAGCC	TTCAATGCCA	CCTTGTTCCCT	GCGCCACATC	CGGAAGCTGG	1140
GGCAGATCCC	AGAGGGCGAG	GGGGCCTCTG	AGCAGGGCAT	GGSCCGNCAC	AGCCACTNAG	1200
GCCTTCGTGC	TGGCCAGCCC	CCCAAGTGGT	GATGCCCAGG	NAGATGCCGA	GGCCAAGTGG	1260

ANTGANCCCC AGATTTNCTT NC

1282

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT03
- (B) CLONE: 1340712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGCGGAGGG	CGCAGGCGGC	TGGGCGCCTG	GCGAGTGGAC	TGTTGAGGCC	CTTCCGCTGG	60
GACCCGGGCC	CTGGCTCCGG	CCCCGCGATG	GGAGCTGCTC	TCCGCGGGCT	GAGCCTGTCA	120
GCATCCTCGA	CGCACCCTGG	TCCCTGAAGT	CGGAGAAGAG	CCCCTACCCA	CCCACACCCC	180
CTTGCCCCAT	TTTGGGTCGC	CTGGGTCTCT	AGTCCTAGCG	GATCCTCAGT	CCTAGCGGCC	240
ACCGGGTCTG	AAAGGAGCAA	GACGATGATC	CTGGCGTCGG	TGCTGAGGAG	CGGTCCCGGG	300
GGCGGGCTTC	CGCTCCGGCC	CCTCCTGGGA	CCCGCACTCG	CGCTCCGGGC	CCGCTCGACG	360
TCGGCCACCG	ACACACACCA	CGTGGAGATG	GCTCGGGAGC	GCTCCAAGAC	CGTCACCTCC	420
TTTTACAACC	AGTCGGCCAT	CGACGCGGCA	GCGGAGAAGC	CCTCAGTCCG	CCTAACGCCC	480
ACCATGATGC	TCTACGCTGG	CCGCTCTCAG	GACGGCAGCC	ACCTTCTGAA	AAGTGCTCGG	540
TACCTGCAGC	AAGAACTTCC	AGTGAGGATT	GCTCACCGCA	TCAAGGGCTT	CCGCTGCCTT	600
CCTTTTCATCA	TTGGCTGCAA	CCCCACCATA	CTGCACGTGC	ATGAGCTATA	TATCCGTGCC	660
TTCCAGAAGC	TGACAGACTT	CCCTCCGATC	AAGGACCAGG	CGGACGAGGC	CCAGTACTGC	720
CAGCTGGTGC	GACAGCTGCT	GGATGACCAC	AAGGATGTGG	TGACCTCTTT	GGCAGAGGGC	780
CTACGTGAGA	GCCGGAAGCA	CATAGAGGAT	GAAAAGCTCG	TCCGCTACTT	CTTGGACAAG	840
ACGCTGACTT	CGAGGCTTGG	AATCCGCATG	TTGGCCACGC	ATCACCTGGC	GCTGCATGAG	900
GACAAGCCTG	ACTTTGTTCG	CATCATCTGT	ACTCGTCTCT	CACCAAAGAA	GATTATTGAG	960
AAGTGGGTGG	ACTTTGCCAG	ACGCCTGTGT	GAGCACAAGT	ATGGCAATGC	GCCCCGTGTC	1020
CGCATCAATG	GCCATGTGGC	TGCCCCGTTT	CCCTTCATCC	CTATGCCACT	GGACTACATC	1080
CTGCCGGAGC	TGCTCAAGAA	TGCCATGAGA	GCCACAATGG	AGAGCCACCT	AGACACTCCC	1140
TACAATGTCC	CAGATGTGGT	CATCACCATG	GCCAACAATG	ATGTGATCTT	GATCATCAGG	1200
ATCTCAGACC	GTGGTGGAGG	AATCGCTCAC	AAAGATCTGG	ACCGGGTCAT	GGACTACCAC	1260
TTCCTACTTG	CTGAGGCCAG	CACACAGGAC	CCCCGGATCA	GCCCCCTCTT	TGGCCATCTG	1320
GACATGCATA	GTGGCGCCCA	GTCAGGACCC	ATGCACGGCT	TTGGCTTCGG	GTTGCCCACG	1380
TCACGGGCCCT	ACGCGGAGTA	CCTCGGTGGG	TCTCTGCAGC	TGCAGTCCCT	GCAGGGCATT	1440
GGCACGGACG	TCTACCTGCG	GCTCCGCCAC	ATCGATGGCC	GGGAGGAAAG	CTTCCGGATC	1500
TGACCCACAC	GCCTTTGGCC	TGCTCACCCG	ACCAGCCTGG	GCCGCATTCC	CTGCAGGACC	1560
TCCCGGGTCA	GGCAGGGCGG	CCCCCTGCTC	CACACACTGC	TGCATCTTGG	GTCTCAGGGA	1620
CCCAGACAGA	TGGACTTACA	TGGAGCTGGG	CACTGCCCTT	GCCTCAACAG	GGTCCATTGC	1680
TCTCTCGCCT	CAGAACTTGG	AGCAGGGAAG	TGGGCACCTG	AGGCCTCAGC	ACAGTGTCTG	1740
CATTCTCTTC	TGGGGGACCC	CACTCTGAGC	TGTTATTAAA	GTTACATTTT	TGGAATGGCC	1800
AGAAAAGAAG	GAAGGTGGAT	GGTGGTGAAG	AGGGGTGGGG	AGAGGTGAGG	TGTTTGTGGT	1860
TTGTGT						1866

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENITUT01
- (B) CLONE: 1452972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCCCCAGCG	CTCGGCCGGC	CGCGAGCCCG	CCGGCCGGGG	ACGAGCGTCG	CAGCTCATGC	60
TGATCGCTGT	CCTCCTCCTC	CCCCTCAGGC	GGCGCTGGCG	GCGGCCCTGG	GACCCGCGGA	120
AGCCGGCATG	CTGGAGAAGC	TGGAGTTCTG	GGACGAAGCA	GTAAGAAGCT	CAGAAAGTGG	180

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TGTTTACATG CGATTTCATGA GGTACACACAA GTGTTATGAC ATCGTTCCAA CCAGTTCAAA 240
GCTTGTGTGTC TTTGATACTA CATTACAAGT TAAAAAGGCC TTCTTTGCTT TGGTAGCCAA 300
CGGTGTCCGA GCAGCGCCAC TGTGGGAGAG TAAAAAACAA AGTTTTGTAG GAATGCTAAC 360
AATTACAGAT TTCATAAATA TACTACATAG ATACTATAAA TCACCTATGG TACAGATTTA 420
TGAATTAGAG GAACATAAAA TTGAAACATG GAGGGAGCTT TATTTACAAG AAACATTTAA 480
GCCTTTAGTG AATATATCTC CAGATGCAAG CCTCTTCGAT GCTGTATACT CCTTGATCAA 540
AAATAAAATC CACAGATTGC CCGTTATTGA CCCTATCAGT GGAATGCAC TTTATATACT 600
TACCCACAAA AGAATCCTCA AGTTCCTCCA GCTTTTTATG TCTGATATGC CAAAGCCTGC 660
CTTCATGAAG CAGAACCTGG ATGAGCTTGG AATAGGAACG TACCACAACA TTGCCTTCAT 720
ACATCCAGAG ACTCCCATCA TCAAAGCCTT GAACATATTT GTGGAAAGAC GAATATCAGC 780
TCTGCCTGTT GTGGATGAGT CAGGAAAAGT TGTAGATATT TATTCCAAAT TTGATGTAAT 840
TAATCTTGCT GCTGAGAAAA CATAACAATA CCTAGATATC ACGGTGACCC AGGCCCTTCA 900
GCACCGTTCA CAGTATTTTG AAGGTGTTGT GAAGTGCAAT AAGCTGGAAA TACTGGAGAC 960
CATCGTGGAC AGAATAGTAA GAGCTGAGGT CCATCGGCTG GTGGTGGTAA ATGAAGCAGA 1020
TAGTATTGTG GGTATTATTT CCCTGTCGGA CATTCGCAA GCCCTGATCC TCACACCAGC 1080
AGGTGCCAAA AAAAAGGAGA CAGAAACGGA GTGACCGCCG TGAATGTAGA CGCCCTAGGA 1140
GGAGAACTTG AACAAAGTCT CTGGGTCACG TTTTGCCTCA TGAACACTGG CTGCAAGTGG 1200
TTAAGAATGT ATATCAGGGT TTAACAATAG GTATTTCCTC CAGTGATGTT GAAATTAAGC 1260
TTAAAAAGA AAGATTTTAT GTGCTTGAAG ATTCAGGCTT GCATTAAAAG ACTGTTTTCA 1320
GACCTTTGTC TGAAGGATTT TAAATGCTGT ATGTCATTAA AGTGCACTGT GTCCTGAAGT 1380
TTTCATTATT TTTCATTTC AAGAATTAC TGGTATGGAA CAGGTGATGT GGCAT 1435

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1488263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Met Leu Ala Gly Leu Pro Thr Ser Asp Pro Gly Arg Leu Ile Thr Asp
 1          5          10          15
Pro Arg Ser Gly Arg Thr Tyr Leu Lys Gly Arg Leu Leu Gly Lys Gly
 20          25          30
Gly Phe Ala Arg Cys Tyr Glu Ala Thr Asp Thr Glu Thr Gly Ser Ala
 35          40          45
Tyr Ala Val Lys Val Ile Pro Gln Ser Arg Val Ala Lys Pro His Gln
 50          55          60
Arg Glu Lys Ile Leu Asn Glu Ile Glu Leu His Arg Asp Leu Gln His
 65          70          75          80
Arg His Ile Val Arg Phe Ser His His Phe Glu Asp Ala Asp Asn Ile
 85          90          95
Tyr Ile Phe Leu Glu Leu Cys Ser Arg Lys Ser Leu Ala His Ile Trp
100          105          110
Lys Ala Arg His Thr Leu Leu Glu Pro Glu Val Arg Tyr Tyr Leu Arg
115          120          125
Gln Ile Leu Ser Gly Leu Lys Tyr Leu His Gln Arg Gly Ile Leu His
130          135          140
Arg Asp Leu Lys Leu Gly Asn Phe Phe Ile Thr Glu Asn Met Glu Leu
145          150          155          160
Lys Val Gly Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Pro Glu Gln
165          170          175
Arg Lys Lys Thr Ile Cys Gly Thr Pro Asn Tyr Val Ala Pro Glu Val
180          185          190
Leu Leu Arg Gln Gly His Gly Pro Glu Ala Asp Val Trp Ser Leu Gly
195          200          205
Cys Val Met Tyr Thr Leu Leu Cys Gly Ser Pro Pro Phe Glu Thr Ala
210          215          220
Asp Leu Lys Glu Thr Tyr Arg Cys Ile Lys Gln Val His Tyr Thr Leu
225          230          235          240

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Pro Ala Ser Leu Ser Leu Pro Ala Arg Gln Leu Leu Ala Ala Ile Leu
      245      250      255
Arg Ala Ser Pro Arg Asp Arg Pro Ser Ile Asp Gln Ile Leu Arg His
      260      265      270
Asp Phe Phe Thr Lys Gly Tyr Thr Pro Asp Arg Leu Pro Ile Ser Ser
      275      280      285
Cys Val Thr Val Pro Asp Leu Thr Pro Pro Asn Pro Ala Arg Ser Leu
      290      295      300
Phe Ala Lys Val Thr Lys Ser Leu Phe Gly Arg Lys Lys Lys Ser Lys
      305      310      315      320
Asn His Ala Gln Glu Arg Asp Glu Val Ser Gly Leu Val Ser Gly Leu
      325      330      335
Met Arg Thr Ser Val Gly His Gln Asp Ala Arg Pro Glu Ala Pro Ala
      340      345      350
Ala Ser Gly Pro Ala Pro Val Ser Leu Val Glu Thr Ala Pro Glu Asp
      355      360      365
Ser Ser Pro Arg Gly Thr Leu Ala Ser Ser Gly Asp Gly Phe Glu Glu
      370      375      380
Gly Leu Thr Val Ala Thr Val Val Glu Ser Ala Leu Cys Ala Leu Arg
      385      390      395      400
Asn Cys Ile Ala Phe Met Pro Pro Ala Glu Gln Asn Pro Ala Pro Leu
      405      410      415
Ala Gln Pro Glu Pro Leu Val Trp Val Ser Lys Trp Val Asp Tyr Ser
      420      425      430
Asn Lys Phe Gly Phe Gly Tyr Gln Leu Ser Ser Arg Arg Val Ala Val
      435      440      445
Leu Phe Asn Asp Gly Thr His Met Ala Leu Ser Ala Asn Arg Lys Thr
      450      455      460
Val His Tyr Asn Pro Thr Ser Thr Lys His Phe Ser Phe Ser Val Gly
      465      470      475      480
Ala Val Pro Arg Ala Leu Gln Pro Gln Leu Gly Ile Leu Arg Tyr Phe
      485      490      495
Ala Ser Tyr Met Glu Gln His Leu Met Lys Gly Gly Asp Leu Pro Ser
      500      505      510
Val Glu Glu Val Glu Val Pro Ala Pro Pro Leu Leu Leu Gln Trp Val
      515      520      525

Lys Thr Asp Gln Ala Leu Leu Met Leu Phe Ser Asp Gly Thr Val Gln
      530      535      540
Val Asn Phe Tyr Gly Asp His Thr Lys Leu Ile Leu Ser Gly Trp Glu
      545      550      555
Pro Leu Leu Val Thr Phe Val Ala Arg Asn Arg Ser Ala Cys Thr Tyr
      565      570      575
Leu Ala Ser His Leu Arg Gln Leu Gly Cys Ser Pro Asp Leu Arg Gln
      580      585      590
Arg Leu Arg Tyr Ala Leu Arg Leu Leu Arg Asp Arg Ser Pro Ala
      595      600      605

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1827450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Pro Arg Val Lys Ala Ala Gln Ala Gly Arg Gln Ser Ser Ala Lys
  1      5      10
Arg His Leu Ala Glu Gln Phe Ala Val Gly Glu Ile Ile Thr Asp Met
      20      25      30

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Ala Lys Lys Glu Trp Lys Val Gly Leu Pro Ile Gly Gln Gly Gly Phe
35 40 45
Gly Cys Ile Tyr Leu Ala Asp Met Asn Ser Ser Glu Ser Val Gly Ser
50 55 60
Asp Ala Pro Cys Val Val Lys Val Glu Pro Ser Asp Asn Gly Pro Leu
65 70 75 80
Phe Thr Glu Leu Lys Phe Tyr Gln Arg Ala Ala Lys Pro Glu Gln Ile
85 90 95
Gln Lys Trp Ile Arg Thr Arg Lys Leu Lys Tyr Leu Gly Val Pro Lys
100 105 110

Tyr Trp Gly Ser Gly Leu His Asp Lys Asn Gly Lys Ser Tyr Arg Phe
115 120 125
Met Ile Met Asp Arg Phe Gly Ser Asp Leu Gln Lys Ile Tyr Glu Ala
130 135 140
Asn Ala Lys Arg Phe Ser Arg Lys Thr Val Leu Gln Leu Ser Leu Arg
145 150 155 160
Ile Leu Asp Ile Leu Glu Tyr Ile His Glu His Glu Tyr Val His Gly
165 170 175
Asp Ile Lys Ala Ser Asn Leu Leu Leu Asn Tyr Lys Asn Pro Asp Gln
180 185 190
Val Tyr Leu Val Asp Tyr Gly Leu Ala Tyr Arg Tyr Cys Pro Glu Gly
195 200 205
Val His Lys Glu Tyr Lys Glu Asp Pro Lys Arg Cys His Asp Gly Thr
210 215 220
Ile Glu Phe Thr Ser Ile Asp Ala His Asn Gly Val Ala Pro Ser Arg
225 230 235 240
Arg Gly Asp Leu Glu Ile Leu Gly Tyr Cys Met Ile Gln Trp Leu Thr
245 250 255
Gly His Leu Pro Trp Glu Asp Asn Leu Lys Asp Pro Lys Tyr Val Arg
260 265 270
Asp Ser Lys Ile Arg Tyr Arg Glu Asn Ile Ala Ser Leu Met Asp Lys
275 280 285
Cys Phe Pro Glu Lys Asn Lys Pro Gly Glu Ile Ala Lys Tyr Met Glu
290 295 300
Thr Val Lys Leu Leu Asp Tyr Thr Glu Lys Pro Leu Tyr Glu Asn Leu
305 310 315 320
Arg Asp Ile Leu Leu Gln Gly Leu Lys Ala Ile Gly Ser Lys Asp Asp
325 330 335
Gly Lys Leu Asp Leu Ser Val Val Glu Asn Gly Gly Leu Lys Ala Lys
340 345 350
Thr Ile Thr Lys Lys Arg Lys Lys Glu Ile Glu Glu Ser Lys Glu Pro
355 360 365
Gly Val Glu Asp Thr Glu Trp Ser Asn Thr Gln Thr Glu Glu Ala Ile
370 375 380
Gln Thr Arg Ser Arg Thr Arg Lys Arg Val Gln Lys
385 390 395

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 303804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro
1 5 10 15
Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala

[illegible][illegible][illegible]

- [illegible]

[illegible]

- [illegible]

[illegible][illegible]

Lys	Glu	Arg	Val	Thr	Met	Thr	Lys	Val	Thr	Leu	Glu	Asn	Phe	Tyr	Ser		
			20					25					30				
Asn	Leu	Ile	Ala	Gln	His	Glu	Glu	Arg	Glu	Met	Arg	Gln	Lys	Lys	Leu		
		35					40					45					
Glu	Lys	Val	Met	Glu	Glu	Glu	Gly	Leu	Lys	Asp	Glu	Glu	Lys	Arg	Leu		
	50					55					60						
Arg	Arg	Ser	Ala	His	Ala	Arg	Lys	Glu	Thr	Glu	Phe	Leu	Arg	Leu	Lys		
65					70					75					80		
Arg	Thr	Arg	Leu	Gly	Leu	Glu	Asp	Phe	Glu	Ser	Leu	Lys	Val	Ile	Gly		
			85						90					95			
Arg	Gly	Ala	Phe	Gly	Glu	Val	Arg	Leu	Val	Gln	Lys	Lys	Asp	Thr	Gly		
		100						105					110				
His	Val	Tyr	Ala	Met	Lys	Ile	Leu	Arg	Lys	Ala	Asp	Met	Leu	Glu	Lys		
		115					120					125					
Glu	Gln	Val	Gly	His	Ile	Arg	Ala	Glu	Arg	Asp	Ile	Leu	Val	Glu	Ala		
	130					135					140						
Asp	Ser	Leu	Trp	Val	Val	Lys	Met	Phe	Tyr	Ser	Phe	Gln	Asp	Lys	Leu		
145					150					155					160		
Asn	Leu	Tyr	Leu	Ile	Met	Glu	Phe	Leu	Pro	Gly	Gly	Asp	Met	Met	Thr		
			165					170						175			
Leu	Leu	Met	Lys	Lys	Asp	Thr	Leu	Thr	Glu	Glu	Glu	Thr	Gln	Phe	Tyr		
		180					185						190				
Ile	Ala	Glu	Thr	Val	Leu	Ala	Ile	Asp	Ser	Ile	His	Gln	Leu	Gly	Phe		
	195					200						205					
Ile	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Leu	Leu	Leu	Asp	Ser	Lys	Gly		
	210				215						220						
His	Val	Lys	Leu	Ser	Asp	Phe	Gly	Leu	Cys	Thr	Gly	Leu	Lys	Lys	Ala		
225					230					235					240		
His	Arg	Thr	Glu	Phe	Tyr	Arg	Asn	Leu	Asn	His	Ser	Leu	Pro	Ser	Asp		
			245					250					255				
Phe	Thr	Phe	Gln	Asn	Met	Asn	Ser	Lys	Arg	Lys	Ala	Glu	Thr	Trp	Lys		
		260				265						270					
Arg	Asn	Arg	Arg	Gln	Leu	Ala	Phe	Ser	Thr	Val	Gly	Thr	Pro	Asp	Tyr		
	275					280						285					
Ile	Ala	Pro	Glu	Val	Phe	Met	Gln	Thr	Gly	Tyr	Asn	Lys	Leu	Cys	Asp		
	290					295					300						
Trp	Trp	Ser	Leu	Gly	Val	Ile	Met	Tyr	Glu	Met	Leu	Ile	Gly	Tyr	Pro		
305				310						315					320		
Pro	Phe	Cys	Ser	Glu	Thr	Pro	Gln	Glu	Thr	Tyr	Lys	Lys	Val	Met	Asn		
			325						330					335			
Trp	Lys	Glu	Thr	Leu	Thr	Phe	Pro	Pro	Glu	Val	Pro	Ile	Ser	Glu	Lys		
		340					345					350					
Ala	Lys	Asp	Leu	Ile	Leu	Arg	Phe	Cys	Cys	Glu	Trp	Glu	His	Arg	Ile		
		355				360						365					
Gly	Ala	Pro	Gly	Val	Glu	Glu	Ile	Lys	Ser	Asn	Ser	Phe	Phe	Glu	Gly		
	370					375					380						
Val	Asp	Trp	Glu	His	Ile	Arg	Glu	Arg	Pro	Ala	Ala	Ile	Ser	Ile	Glu		
385					390					395					400		
Ile	Lys	Ser	Ile	Asp	Asp	Thr	Ser	Asn	Phe	Asp	Glu	Phe	Pro	Glu	Ser		
			405						410					415			
Asp	Ile	Leu	Lys	Pro	Thr	Val	Ala	Thr	Ser	Asn	His	Pro	Glu	Thr	Asp		
		420						425					430				
Tyr	Lys	Asn	Lys	Asp	Trp	Val	Phe	Ile	Asn	Tyr	Thr	Tyr	Lys	Arg	Phe		
		435				440						445					
Glu	Gly	Leu	Thr	Ala	Arg	Gly	Ala	Ile	Pro	Ser	Tyr	Met	Lys	Ala	Ala		
	450					455					460						
Lys																	
465																	

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(B) CLONE: 790790

[illegible]

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 924921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser	Thr	Ser	Ala	Thr	Asp	Thr	His	His	Val	Glu	Leu	Ala	Arg	Glu	Arg
1				5					10					15	
Ser	Lys	Thr	Val	Thr	Ser	Phe	Tyr	Asn	Gln	Ser	Ala	Ile	Asp	Val	Val
			20					25					30		
Ala	Glu	Lys	Pro	Ser	Val	Arg	Leu	Thr	Pro	Thr	Met	Met	Leu	Tyr	Ser
		35					40					45			
Gly	Arg	Ser	Gln	Asp	Gly	Ser	His	Leu	Leu	Lys	Ser	Gly	Arg	Tyr	Leu
	50					55					60				
Gln	Gln	Glu	Leu	Pro	Val	Arg	Ile	Ala	His	Arg	Ile	Lys	Gly	Phe	Arg
65					70					75					80
Ser	Leu	Pro	Phe	Ile	Ile	Gly	Cys	Asn	Pro	Thr	Ile	Leu	His	Val	His
				85				90						95	
Glu	Leu	Tyr	Ile	Arg	Ala	Phe	Gln	Lys	Leu	Thr	Asp	Phe	Pro	Pro	Ile
			100					105					110		
Lys	Asp	Gln	Ala	Asp	Glu	Ala	Gln	Tyr	Cys	Gln	Leu	Val	Arg	Gln	Leu
		115					120					125			
Leu	Asp	Asp	His	Lys	Asp	Val	Val	Thr	Leu	Leu	Ala	Glu	Gly	Leu	Arg
	130					135					140				
Glu	Ser	Arg	Lys	His	Ile	Glu	Asp	Glu	Lys	Leu	Val	Arg	Tyr	Phe	Leu
145					150					155					160
Asp	Lys	Thr	Leu	Thr	Ser	Arg	Leu	Gly	Ile	Arg	Met	Leu	Ala	Thr	His
			165					170						175	
His	Leu	Ala	Leu	His	Glu	Asp	Lys	Pro	Asp	Phe	Val	Gly	Ile	Ile	Cys
		180						185					190		
Thr	Arg	Leu	Ser	Pro	Lys	Lys	Ile	Ile	Glu	Lys	Trp	Val	Asp	Phe	Ala
	195					200						205			
Arg	Arg	Leu	Cys	Glu	His	Lys	Tyr	Gly	Asn	Ala	Pro	Arg	Val	Arg	Ile
	210					215					220				
Asn	Gly	His	Val	Ala	Ala	Arg	Phe	Pro	Phe	Ile	Pro	Met	Pro	Leu	Asp
225				230						235					240
Tyr	Ile	Leu	Pro	Glu	Leu	Leu	Lys	Asn	Ala	Met	Arg	Ala	Thr	Met	Glu
			245					250					255		
Ser	His	Leu	Asp	Thr	Pro	Tyr	Asn	Val	Pro	Asp	Val	Val	Ile	Thr	Ile
		260					265						270		
Ala	Asn	Asn	Asp	Val	Asp	Leu	Ile	Ile	Arg	Ile	Ser	Asp	Arg	Gly	Gly
		275				280						285			
Gly	Ile	Ala	His	Lys	Asp	Leu	Asp	Arg	Val	Met	Asp	Tyr	His	Phe	Thr
	290					295				300					
Thr	Ala	Glu	Ala	Ser	Thr	Gln	Asp	Pro	Arg	Ile	Ser	Pro	Leu	Phe	Gly
305					310					315					320
His	Leu	Asp	Met	His	Ser	Gly	Gly	Gln	Ser	Gly	Pro	Met	His	Gly	Phe
			325					330						335	
Gly	Phe	Gly	Leu	Pro	Thr	Ser	Arg	Ala	Tyr	Ala	Glu	Tyr	Leu	Gly	Gly
		340						345					350		
Ser	Leu	Gln	Leu	Gln	Ser	Leu	Gln	Gly	Ile	Gly	Thr	Asp	Val	Tyr	Leu
	355					360						365			
Arg	Leu	Arg	His	Ile	Asp	Gly	Arg	Glu	Glu	Ser	Phe	Arg	Ile		
	370					375						380			

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 1335856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Glu	Thr	Val	Ile	Ser	Ser	Asp	Ser	Ser	Pro	Ala	Val	Glu	Asn	Glu	1	5	10	15
His	Pro	Gln	Glu	Thr	Pro	Glu	Ser	Asn	Asn	Ser	Val	Tyr	Thr	Ser	Phe	20	25	30	
Met	Lys	Ser	His	Arg	Cys	Tyr	Asp	Leu	Ile	Pro	Thr	Ser	Ser	Lys	Leu	35	40	45	
Val	Val	Phe	Asp	Thr	Ser	Leu	Gln	Val	Lys	Lys	Ala	Phe	Phe	Ala	Leu	50	55	60	
Val	Thr	Asn	Gly	Val	Arg	Ala	Ala	Pro	Leu	Trp	Asp	Ser	Lys	Lys	Gln	65	70	75	80
Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Asn	Ile	Leu	His	85	90	95	
Arg	Tyr	Tyr	Lys	Ser	Ala	Leu	Val	Gln	Ile	Tyr	Glu	Leu	Glu	Glu	His	100	105	110	
Lys	Ile	Glu	Thr	Trp	Arg	Glu	Val	Tyr	Leu	Gln	Asp	Ser	Phe	Lys	Pro	115	120	125	
Leu	Val	Cys	Ile	Ser	Pro	Asn	Ala	Ser	Leu	Phe	Asp	Ala	Val	Ser	Ser	130	135	140	
Leu	Ile	Arg	Asn	Lys	Ile	His	Arg	Leu	Pro	Val	Ile	Asp	Pro	Glu	Ser	145	150	155	160
Gly	Asn	Thr	Leu	Tyr	Ile	Leu	Thr	His	Lys	Arg	Ile	Leu	Lys	Phe	Leu	165	170	175	
Lys	Leu	Phe	Ile	Thr	Glu	Phe	Pro	Lys	Pro	Glu	Phe	Met	Ser	Lys	Ser	180	185	190	
Leu	Glu	Glu	Leu	Gln	Ile	Gly	Thr	Tyr	Ala	Asn	Ile	Ala	Met	Val	Arg	195	200	205	
Thr	Thr	Thr	Pro	Val	Tyr	Val	Ala	Leu	Gly	Ile	Phe	Val	Gln	His	Arg	210	215	220	
Val	Ser	Ala	Leu	Pro	Val	Val	Asp	Glu	Lys	Gly	Arg	Val	Val	Asp	Ile	225	230	235	240
Tyr	Ser	Lys	Phe	Asp	Val	Ile	Asn	Leu	Ala	Ala	Glu	Lys	Thr	Tyr	Asn	245	250	255	
Asn	Leu	Asp	Val	Ser	Val	Thr	Lys	Ala	Leu	Gln	His	Arg	Ser	His	Tyr	260	265	270	
Phe	Glu	Gly	Val	Leu	Lys	Cys	Tyr	Leu	His	Glu	Thr	Leu	Glu	Thr	Ile	275	280	285	
Ile	Asn	Arg	Leu	Val	Glu	Ala	Glu	Val	His	Arg	Leu	Val	Val	Val	Asp	290	295	300	
Glu	Asn	Asp	Val	Val	Lys	Gly	Ile	Val	Ser	Leu	Ser	Asp	Ile	Leu	Gln	305	310	315	320
Ala	Leu	Val	Leu	Thr	Gly	Gly	Glu	Lys	Lys	Pro						325	330		